

<!--StartFragment-->GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 29, 2008, 14:08:24 ; Search time 532 Seconds
(without alignments)
2415.068 Million cell updates/sec

Title: US-10-532-944-8

Perfect score: 4230

Sequence: 1 MGMIHEQTDFTTSEAIRPDT.....FTPDDVREARAQGISFSIHV 781

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5032670 seqs, 1645091341 residues

Total number of hits satisfying chosen parameters: 5032670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_12.1:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3937	93.1	728	2	Q9RHZ2_ALIAC	Q9rhz2 alicyclobac
2	1937	45.8	787	1	AGL2_BACTQ	Q9f234 bacillus th
3	1888	44.6	779	2	Q2B942_9BACI	Q2b942 bacillus sp
4	1739.5	41.1	801	2	Q2AET1_9FIRM	Q2aet1 halothermot
5	1670	39.5	763	2	Q724N0_LISMF	Q724n0 listeria mo
6	1665.5	39.4	764	2	A4DZ14_LISMO	A4dz14 listeria mo
7	1665	39.4	763	2	Q8YAE7_LISMO	Q8yae7 listeria mo
8	1663	39.3	763	2	A3GEH3_LISMO	A3geh3 listeria mo
9	1663	39.3	763	2	A4DI93_LISMO	A4di93 listeria mo
10	1662.5	39.3	763	2	Q4EI93_LISMO	Q4ei93 listeria mo
11	1659.5	39.2	764	2	A4DAQ6_LISMO	A4daq6 listeria mo
12	1653.5	39.1	763	2	Q92F84_LISIN	Q92f84 listeria in
13	1651.5	39.0	763	2	A3FXQ0_LISMO	A3fxq0 listeria mo
14	1651.5	39.0	763	2	Q4ERP5_LISMO	Q4erp5 listeria mo
15	1651.5	39.0	763	2	A4DR94_LISMO	A4dr94 listeria mo
16	1651.5	39.0	763	2	A3FYZ7_LISMO	A3fyz7 listeria mo
17	1531	36.2	803	2	Q1AU85_RUBXD	Q1au85 rubrobacter
18	1506	35.6	281	2	Q9WX33_ALIAC	Q9wx33 alicyclobac
19	1475	34.9	808	2	A0NI45_OENOE	A0ni45 oenococcus
20	1457	34.4	790	2	A6LTE1_CLOBE	A6ltel clostridium

21	1453.5	34.4	752	2	Q0ERR0_THEET	Q0err0 thermoanaer
22	1453	34.3	782	2	A4BEH4_9GAMM	A4beh4 reinekea sp
23	1452	34.3	811	2	Q2JSE3_SYNJA	Q2jse3 synechococc
24	1451.5	34.3	752	2	Q3CJW2_THEET	Q3cjw2 thermoanaer
25	1451	34.3	751	2	Q8RDL1_THETN	Q8rdl1 thermoanaer
26	1436.5	34.0	820	2	Q2JLQ6_SYNJB	Q2j1q6 synechococc
27	1430.5	33.8	752	2	A6NAA1_THEET	A6naa1 thermoanaer
28	1402	33.1	828	2	Q1ITZ5_ACIBL	Q1itz5 acidobacter
29	1398.5	33.1	779	2	Q8YN00_ANASP	Q8yn00 anabaena sp
30	1397	33.0	756	2	Q0LC91_HERAU	Q0lc91 herpetosiph
31	1396.5	33.0	799	2	Q099U6_STIAU	Q099u6 stigmatella
32	1381.5	32.7	768	2	Q74HN8_LACJO	Q74hn8 lactobacill
33	1371.5	32.4	776	2	Q7NP60_GLOVI	Q7np60 gloeobacter
34	1368.5	32.4	767	2	Q5FI60_LACAC	Q5fi60 lactobacill
35	1358	32.1	792	2	Q040V5_LACGA	Q040v5 lactobacill
36	1349	31.9	768	2	Q1UA36_LACRE	Q1ua36 lactobacill
37	1348	31.9	768	2	A5VKA3_LACRE	A5vka3 lactobacill
38	1344	31.8	768	2	Q0GL90_LACRE	Q0gl90 lactobacill
39	1341.5	31.7	814	2	Q3DX78_CHLAU	Q3dx78 chloroflexu
40	1339	31.7	825	2	A0H583_9CHLR	A0h583 chloroflexu
41	1337.5	31.6	766	2	Q88SA1_LACPL	Q88sal lactobacill
42	1335.5	31.6	823	2	A6E786_9SPHI	A6e786 pedobacter
43	1328.5	31.4	798	2	Q091G4_STIAU	Q091g4 stigmatella
44	1313.5	31.1	845	2	Q2B3F7_9BACI	Q2b3f7 bacillus sp
45	1299	30.7	746	2	Q8XIN9_CLOPE	Q8xin9 clostridium

ALIGNMENTS

RESULT 1

Q9RHZ2_ALIAC

ID Q9RHZ2_ALIAC Unreviewed; 728 AA.
 AC Q9RHZ2;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 24-JUL-2007, entry version 22.
 DE Putative alpha-glucosidase.
 GN Name=glcA;
 OS Alicyclobacillus acidocaldarius (Bacillus acidocaldarius).
 OC Bacteria; Firmicutes; Bacillales; Alicyclobacillaceae;
 OC Alicyclobacillus.
 OX NCBI_TaxID=1388;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 27009;
 RX MEDLINE=20507797; PubMed=11053372;
 RX DOI=10.1128/JB.182.22.6292-6301.2000;
 RA Hulsmann A., Lurz R., Scheffel F., Schneider E.;
 RT "Maltose and maltodextrin transport in the thermoacidophilic gram-
 RT positive bacterium Alicyclobacillus acidocaldarius is mediated by a
 RT high-affinity transport system that includes a maltose binding protein
 RT tolerant to low pH.";
 RL J. Bacteriol. 182:6292-6301(2000).
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 DR EMBL; AJ252161; CAB65656.1; -; Genomic_DNA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA:InterPro.
 DR GO; GO:0005975; P:carbohydrate metabolic process; IEA:InterPro.

DR InterPro; IPR000322; Glyco_hydro_31.
 DR PANTHER; PTHR22762; Glyco_hydro_31; 1.
 DR Pfam; PF01055; Glyco_hydro_31; 1.
 DR PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
 PE 4: Predicted;
 SQ SEQUENCE 728 AA; 82972 MW; 49FC605F929409A0 CRC64;

Query Match 93.1%; Score 3937; DB 2; Length 728;
 Best Local Similarity 100.0%; Pred. No. 3.2e-289;
 Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 MVGVAALDDTVLRVAYCRSPGEWPTSTPAIVEQMSQRHSWRLVQEERRVQLECVAGWQIQ 113
 |||||||
 Db 1 MVGVAALDDTVLRVAYCRSPGEWPTSTPAIVEQMSQRHSWRLVQEERRVQLECVAGWQIQ 60

Qy 114 INRDDGTWSIRHLGFGTAVEAITWYKRKKGGALTFASLDNARFYGLGEKPGPLDKRHEAY 173
 |||||||
 Db 61 INRDDGTWSIRHLGFGTAVEAITWYKRKKGGALTFASLDNARFYGLGEKPGPLDKRHEAY 120

Qy 174 TMWNSDVFYAPHVPEMEALYLSIPFFLRLQDQTAVGIFVDNPGRSRFDFRSRYPDVEISTE 233
 |||||||
 Db 121 TMWNSDVFYAPHVPEMEALYLSIPFFLRLQDQTAVGIFVDNPGRSRFDFRSRYPDVEISTE 180

Qy 234 RGGLDVYFIFGASLKDViRRYTKLTGRMPMPPK WALGYHQSRYSYETQSEVLSVAQTFVE 293
 |||||||
 Db 181 RGGLDVYFIFGASLKDViRRYTKLTGRMPMPPK WALGYHQSRYSYETQSEVLSVAQTFVE 240

Qy 294 RDIPVDALYLDIHMDGYRVFTFDERRFPDPARMCD ELRKLGVVVPIVDPGVKQDPEYP 353
 |||||||
 Db 241 RDIPVDALYLDIHMDGYRVFTFDERRFPDPARMCD ELRKLGVVVPIVDPGVKQDPEYP 300

Qy 354 VYMDGLAHNF CQTAEGQVYLGEVWPGLSAFPDFASEEVRAWWGKWHRVYTQMGIEGIWN 413
 |||||||
 Db 301 VYMDGLAHNF CQTAEGQVYLGEVWPGLSAFPDFASEEVRAWWGKWHRVYTQMGIEGIWN 360

Qy 414 DMNEPAVFNETKMDVNVVHRGDGR LYTHGEVHNLYGFWM AETYRGLKAQLAGKRPFVL 473
 |||||||
 Db 361 DMNEPAVFNETKMDVNVVHRGDGR LYTHGEVHNLYGFWM AETYRGLKAQLAGKRPFVL 420

Qy 474 TRAGYSGIQR YAAWTGDNRSFWEHMAMAIPMV LNMMSGIPLGGPDVGGFAHHAS GELL 533
 |||||||
 Db 421 TRAGYSGIQR YAAWTGDNRSFWEHMAMAIPMV LNMMSGIPLGGPDVGGFAHHAS GELL 480

Qy 534 ARWTQMGAFFPFRNHSAMGTHRQE PWA FGPTFEAVIRRAIRLRYRFLPYLYTLAREAHE 593
 |||||||
 Db 481 ARWTQMGAFFPFRNHSAMGTHRQE PWA FGPTFEAVIRRAIRLRYRFLPYLYTLAREAHE 540

Qy 594 TGLPMMRPLVLEY PDDPNTHVDDQFLVGS DLLVAPILKPGMAHRM VYLPDGEWIDYETR 653
 |||||||
 Db 541 TGLPMMRPLVLEY PDDPNTHVDDQFLVGS DLLVAPILKPGMAHRM VYLPDGEWIDYETR 600

Qy 654 ERYQGRQYILTYAPLDRIP LYVRAGSAIPVNLLERSGETQLGWEIFVDANGRASGR CYED 713
 |||||||
 Db 601 ERYQGRQYILTYAPLDRIP LYVRAGSAIPVNLLERSGETQLGWEIFVDANGRASGR CYED 660

Qy 714 DGETFSYEDGAYCDRVLQALATSEGTLIECHLVQGSGDGG SLES VV RVFTPDDVREARAQ 773
 |||||||
 Db 661 DGETFSYEDGAYCDRVLQALATSEGTLIECHLVQGSGDGG SLES VV RVFTPDDVREARAQ 720

Qy 774 GISFSIHV 781
 |||||||

Db 721 GISFSIHV 728

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